



1/7

SEQUENCE LISTING

<110> Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

10 <130> 77813-49

<140> to be assigned

<141>

<150> US 60/194,464

<151> 2000-04-04

<160> 7

20 <170> PatentIn Ver. 2.0

<210> 1

<211> 1799

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

30 <222> (101)..(1696)

<400> 1

acttcccccc tgctaaacta tgctcagata atgctgctat gattgcaggt ctagggggag 60

aaaattttca aaaaaactct agtattccgg aaattcgtat atg cgc aag ata tca 115  
Met Arg Lys Ile Ser  
1 5

40 gtg gga atc tgt atc acc att ctc ctt agc ctc tcc gta gtc ctc caa 163  
Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu Ser Val Val Leu Gln  
10 15 20

ggc tgc aag gag tcc agt cac tcc tct aca tct cgg gga gaa ctc gct 211  
Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser Arg Gly Glu Leu Ala  
25 30 35

att aat ata aga gat gaa ccc cgt tct tta gat cca aga caa gtg cga 259  
Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp Pro Arg Gln Val Arg  
40 45 50

50 ctt ctt tca gaa atc agc ctt gtc aaa cat atc tat gag gga tta gtt 307  
Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile Tyr Glu Gly Leu Val  
55 60 65

caa gaa aat aat ctt tca gga aat ata gag cct gct ctt gca gaa gac 355  
Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro Ala Leu Ala Glu Asp  
70 75 80 85

60 tac tct ctt tcc tcg gac gga ctc act tat act ttt aaa ctg aaa tca 403  
Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr Phe Lys Leu Lys Ser  
90 95 100

2/7

|    |   |      |
|----|---|------|
|    | gct ttt tgg agt aat ggc gac ccc tta aca gct gaa gac ttt ata gaa | 451  |
|    | Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala Glu Asp Phe Ile Glu |      |
|    | 105 110 115   |      |
|    | tct tgg aaa caa gta gct act caa gaa gtc tca gga atc tat gct ttt | 499  |
|    | Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser Gly Ile Tyr Ala Phe |      |
|    | 120 125 130   |      |
| 10 | gcc ttg aat cca att aaa aat gta cga aag atc caa gag gga cac ctc | 547  |
|    | Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile Gln Glu Gly His Leu |      |
|    | 135 140 145   |      |
|    | tcc ata gac cat ttt gga gtg cac tct cct aat gaa tct aca ctt gtt | 595  |
|    | Ser Ile Asp His Phe Gly Val His Ser Pro Asn Glu Ser Thr Leu Val |      |
|    | 150 155 160 165   |      |
| 20 | gtt acc ctg gaa tcc cca acc tcg cat ttc tta aaa ctt tta gct ctt | 643  |
|    | Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu Lys Leu Leu Ala Leu |      |
|    | 170 175 180   |      |
|    | cca gtc ttt ttc ccc gtt cat aaa tct caa aga acc ctg caa tcc aaa | 691  |
|    | Pro Val Phe Phe Pro Val His Lys Ser Gln Arg Thr Leu Gln Ser Lys |      |
|    | 185 190 195   |      |
|    | tct cta cct ata gca agc gga gct ttc tat cct aaa aat atc aaa caa | 739  |
|    | Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro Lys Asn Ile Lys Gln |      |
|    | 200 205 210   |      |
| 30 | aaa caa tgg ata aaa ctc tca aaa aac cct cac tac tat aat caa agt | 787  |
|    | Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His Tyr Tyr Asn Gln Ser |      |
|    | 215 220 225   |      |
|    | cag gtg gaa act aaa acg att acg att cac ttc att ccc gat gca aac | 835  |
|    | Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe Ile Pro Asp Ala Asn |      |
|    | 230 235 240 245   |      |
| 40 | aca gca gca aaa cta ttt aat cag gga aaa ctc aat tgg caa gga cct | 883  |
|    | Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu Asn Trp Gln Gly Pro |      |
|    | 250 255 260   |      |
|    | cct tgg gga gaa cgc att cct caa gaa acc cta tcc aat tta cag tct | 931  |
|    | Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu Ser Asn Leu Gln Ser |      |
|    | 265 270 275   |      |
|    | aag ggg cac tta cac tct ttt gat gtc gca gga acc tca tgg ctc acc | 979  |
|    | Lys Gly His Leu His Ser Phe Asp Val Ala Gly Thr Ser Trp Leu Thr |      |
|    | 280 285 290   |      |
| 50 | ttc aat atc aat aaa ttc ccc ctc aac aat atg aag ctt aga gaa gcc | 1027 |
|    | Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met Lys Leu Arg Glu Ala |      |
|    | 295 300 305   |      |
|    | tta gca tca gcc tta gat aag gaa gct ctt gtc tca act ata ttc tta | 1075 |
|    | Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val Ser Thr Ile Phe Leu |      |
|    | 310 315 320 325   |      |
| 60 | ggc cgt gca aaa act gcc gat cat ctc cta cct aca aat att cat agc | 1123 |
|    | Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro Thr Asn Ile His Ser |      |
|    | 330 335 340   |      |

3/7

|    |   |      |
|----|---|------|
|    | tat ccc gaa cat caa aaa caa gag atg gca caa cgc caa gct tac gct   | 1171 |
|    | Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln Arg Gln Ala Tyr Ala   |      |
|    | 345 350 355   |      |
|    | aaa aaa ctc ttt aaa gaa gct tta gaa gaa ctc caa atc act gct aaa   | 1219 |
|    | Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu Gln Ile Thr Ala Lys   |      |
|    | 360 365 370   |      |
| 10 | gat ctc gaa cat ctt aat ctt atc ttt ccc gtt tcc tcg tca gca agt   | 1267 |
|    | Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val Ser Ser Ala Ser       |      |
|    | 375 380 385   |      |
|    | tct tta cta gtc caa ctt ata cga gaa cag tgg aaa gaa agt tta ggg   | 1315 |
|    | Ser Leu Leu Val Gln Leu Ile Arg Glu Gln Trp Lys Glu Ser Leu Gly   |      |
|    | 390 395 400 405   |      |
| 20 | ttc gct atc cct att gtc gga aag gaa ttt gct ctt ctc caa gca gac   | 1363 |
|    | Phe Ala Ile Pro Ile Val Gly Lys Glu Phe Ala Leu Leu Gln Ala Asp   |      |
|    | 410 415 420   |      |
|    | cta tct tca ggg aac ttc tct tta gct aca gga gga tgg ttc gca gac   | 1411 |
|    | Leu Ser Ser Gly Asn Phe Ser Leu Ala Thr Gly Gly Trp Phe Ala Asp   |      |
|    | 425 430 435   |      |
|    | ttt gct gat cct atg gca ttt cta acg atc ttt gct tat cca tca gga   | 1459 |
|    | Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe Ala Tyr Pro Ser Gly   |      |
|    | 440 445 450   |      |
| 30 | gtt cct cct tat gca atc aac cat aag gac ttc cta gaa att cta caa   | 1507 |
|    | Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe Leu Glu Ile Leu Gln   |      |
|    | 455 460 465   |      |
|    | aac ata gaa caa gag caa gat cac caa aaa cgc tcg gaa tta gtg tcg   | 1555 |
|    | Asn Ile Glu Gln Glu Gln Asp His Gln Lys Arg Ser Glu Leu Val Ser   |      |
|    | 470 475 480 485   |      |
| 40 | caa gct tct ctt tac cta gag acc ttt cat att att gag ccg atc tac   | 1603 |
|    | Gln Ala Ser Leu Tyr Leu Glu Thr Phe His Ile Ile Glu Pro Ile Tyr   |      |
|    | 490 495 500   |      |
|    | cac gac gca ttt caa ttt gct atg aat aaa aaa ctt tct aat cta gga   | 1651 |
|    | His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys Leu Ser Asn Leu Gly   |      |
|    | 505 510 515   |      |
|    | gtc tca cca aca gga gtt gtg gac ttc cgt tat gct aag gaa aat       | 1696 |
|    | Val Ser Pro Thr Gly Val Val Asp Phe Arg Tyr Ala Lys Glu Asn       |      |
|    | 520 525 530   |      |
| 50 | tagcacctct tttaatctcg caaacttgtc aagaactgaa tcttatacta aactgggtgc | 1756 |
|    | ctttgtggca cctcgtttcc ttctgactgc tcttctctct cta                   | 1799 |

<210> 2

<211> 532

<212> PRT

<213> Chlamydia pneumoniae

60

<220>

<221> SITE

<222> (53)...(61)  
<223> T-cell epitope

<220>  
<221> SITE  
<222> (338)...(359)  
<223> B-cell epitope

10

<220>  
<221> SITE  
<222> (469)...(482)  
<223> B-cell epitope

<400> 2

Met Arg Lys Ile Ser Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu  
1 5 10 15

20 Ser Val Val Leu Gln Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser  
20 25 30

Arg Gly Glu Leu Ala Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp  
35 40 45

Pro Arg Gln Val Arg Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile  
50 55 60

30 Tyr Glu Gly Leu Val Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro  
65 70 75 80

Ala Leu Ala Glu Asp Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr  
85 90 95

Phe Lys Leu Lys Ser Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala  
100 105 110

Glu Asp Phe Ile Glu Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser  
115 120 125

40

Gly Ile Tyr Ala Phe Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile  
130 135 140

Gln Glu Gly His Leu Ser Ile Asp His Phe Gly Val His Ser Pro Asn  
145 150 155 160

Glu Ser Thr Leu Val Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu  
165 170 175

50 Lys Leu Leu Ala Leu Pro Val Phe Phe Pro Val His Lys Ser Gln Arg  
180 185 190

Thr Leu Gln Ser Lys Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro  
195 200 205

Lys Asn Ile Lys Gln Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His  
210 215 220

60 Tyr Tyr Asn Gln Ser Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe  
225 230 235 240

Ile Pro Asp Ala Asn Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu  
245 250 255

Asn Trp Gln Gly Pro Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu  
260 265 270

10 Ser Asn Leu Gln Ser Lys Gly His Leu His Ser Phe Asp Val Ala Gly  
275 280 285

Thr Ser Trp Leu Thr Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met  
290 295 300

Lys Leu Arg Glu Ala Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val  
305 310 315 320

Ser Thr Ile Phe Leu Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro  
325 330 335

20 Thr Asn Ile His Ser Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln  
340 345 350

Arg Gln Ala Tyr Ala Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu  
355 360 365

Gln Ile Thr Ala Lys Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val  
370 375 380

30 Ser Ser Ser Ala Ser Ser Leu Leu Val Gln Leu Ile Arg Glu Gln Trp  
385 390 395 400

Lys Glu Ser Leu Gly Phe Ala Ile Pro Ile Val Gly Lys Glu Phe Ala  
405 410 415

Leu Leu Gln Ala Asp Leu Ser Ser Gly Asn Phe Ser Leu Ala Thr Gly  
420 425 430

Gly Trp Phe Ala Asp Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe  
435 440 445

40 Ala Tyr Pro Ser Gly Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe  
450 455 460

Leu Glu Ile Leu Gln Asn Ile Glu Gln Glu Gln Asp His Gln Lys Arg  
465 470 475 480

Ser Glu Leu Val Ser Gln Ala Ser Leu Tyr Leu Glu Thr Phe His Ile  
485 490 495

50 Ile Glu Pro Ile Tyr His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys  
500 505 510

Leu Ser Asn Leu Gly Val Ser Pro Thr Gly Val Val Asp Phe Arg Tyr  
515 520 525

Ala Lys Glu Asn  
530

<210> 3  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' PCR primer

10

<400> 3  
ataagaatgc ggccgccacc atgcgcaaga tatcagtggg aatc 44

<210> 4  
<211> 37  
<212> DNA  
<213> Artificial Sequence

20

<220>  
<223> 3' PCR primer

<400> 4  
gcgcccggatc ccattttcct tagcataacg gaagtcc 37

<210> 5  
<211> 22  
<212> PRT  
<213> Artificial Sequence

30

<220>  
<223> B-cell epitope

<400> 5  
Asn Ile His Ser Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln  
5 10 15

40 Arg Gln Ala Tyr Ala Lys Lys  
20

<210> 6  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> B-cell epitope

50

<400> 6  
Gln Asn Ile Glu Gln Glu Gln Asp His Gln Lys Arg Ser Glu  
5 10

<210> 7  
<211> 9  
<212> PRT  
<213> Artificial Sequence

60

Atty. Docket No. 032931/0246

Inventor: Andrew MURDIN et al.

Serial No.: 09/824,567

7/7

<220>

<223> T-cell epitope

<400> 7

Arg Leu Leu Ser Glu Ile Ser Leu Val

5